High Throughput Computational methods, Metabolic manipulation, and Analysis of gene manipulation.

Although it is possible to generate vast quantities of experimental data, there remains a need for tools to facilitate high throughput analysis of this data.

MEWG Workshop Topic 3
Feb. 14th 2006

Moderator: Michael J. Betenbaugh
Johns Hopkins University

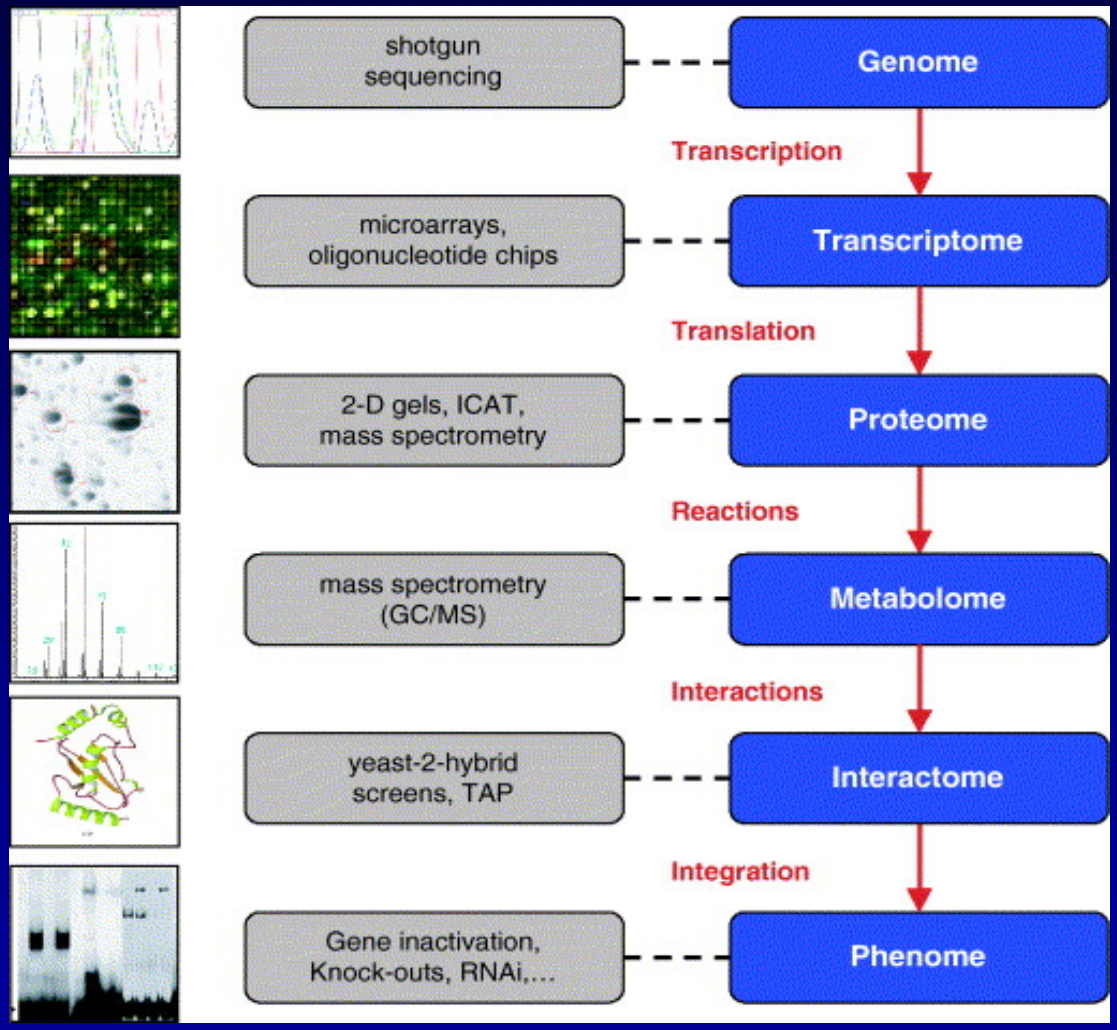
Question 1: How can genomics enable us to target specific genes ?

What are the experimental tools of genomics?

How can these specify particular genes of interest?

Question 1: How can genomics enable us to target specific genes ?

Tools?
Analytical Methods?



Fischer: Biotech. Annual Review, 2005

Question 2:

What computational tools will allow us to evaluate and/or predict manipulations in silico?

- **Databases**
  - **Genomic-Proteomic-Microarray-Metabolome**
- **Analytical Tools**
  - **Normalization and Data quality**
  - **Inference**
  - **Classification**
- **Computational Models**
  - **Regulatory Networks**
  - **Metabolic models**

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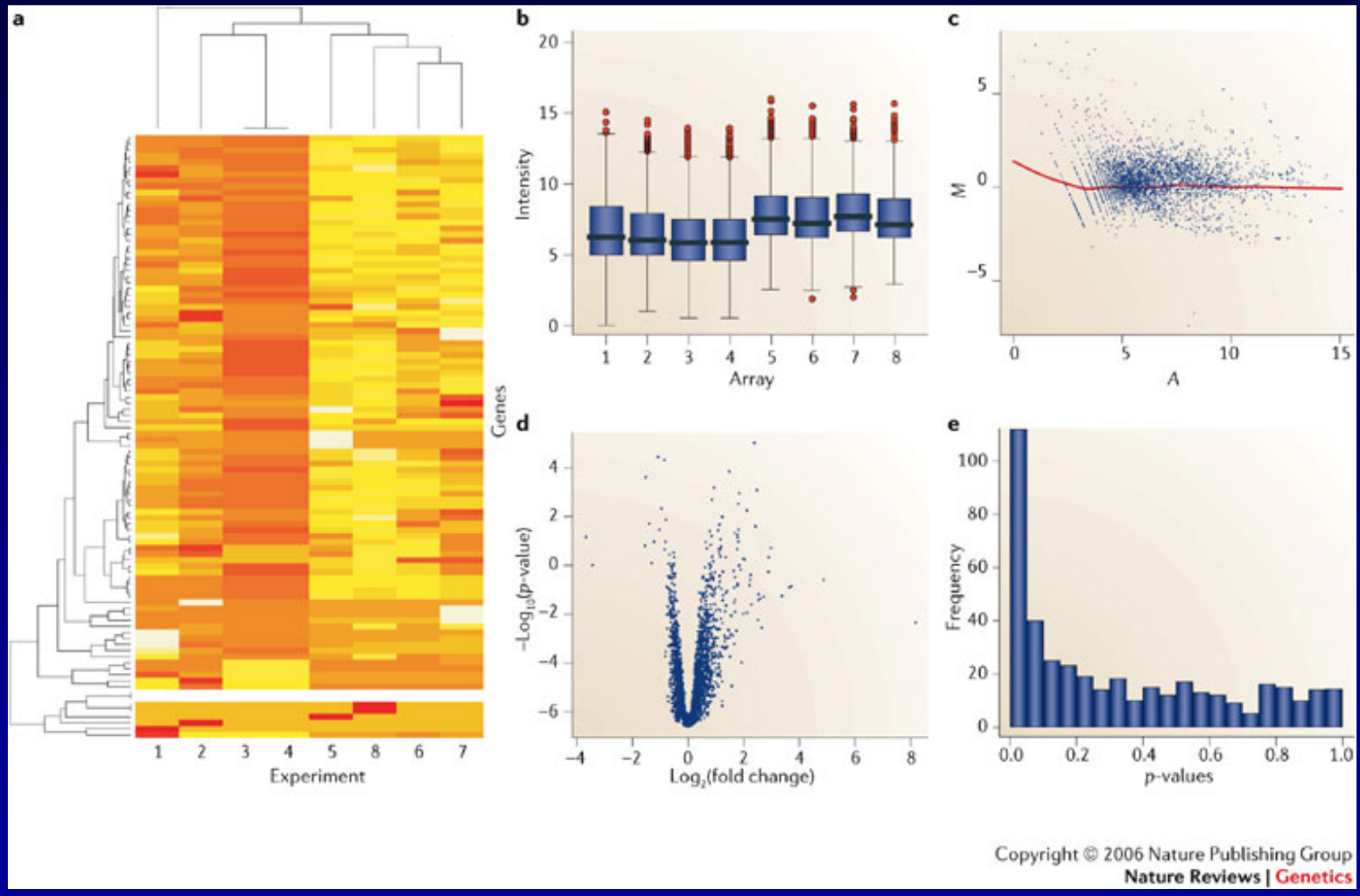

Allison DB *et al.* (2005) Microarray data analysis: from disarray to consolidation and consensus *Nat Rev gene.* **7:** 55–65 doi:10.1038/nri1749

Question 3:

What HTP tools are needed to experimentally evaluate or validate predicted changes in gene or metabolic manipulation?

- cDNA microarrays
- Protein chips and proteomics
- Metabolic assays
- Cell based functional assays
  - siRNA
  - Overexpression
  - Functional assays
  - Electron microscopy and localization assays
- In vivo models

Question 3:

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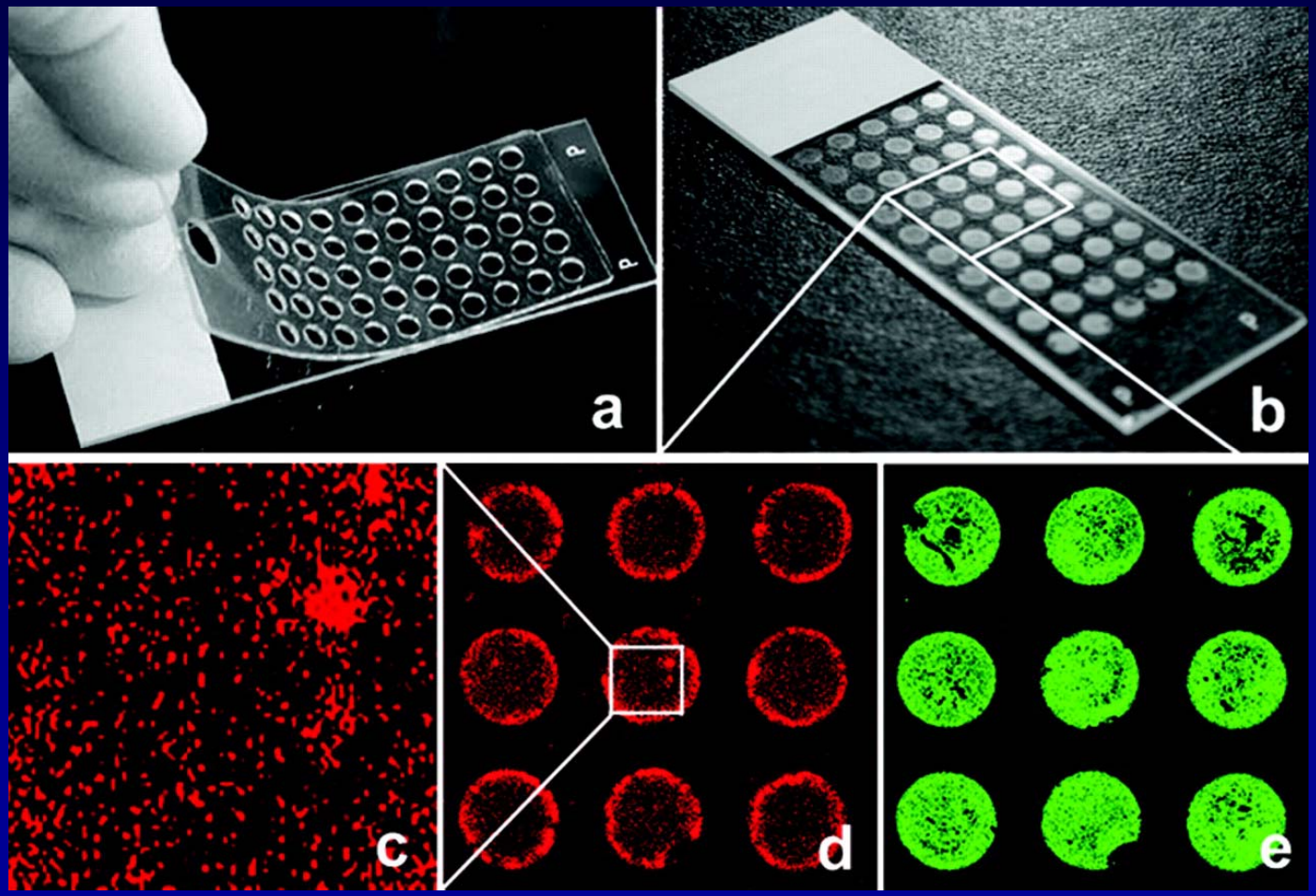

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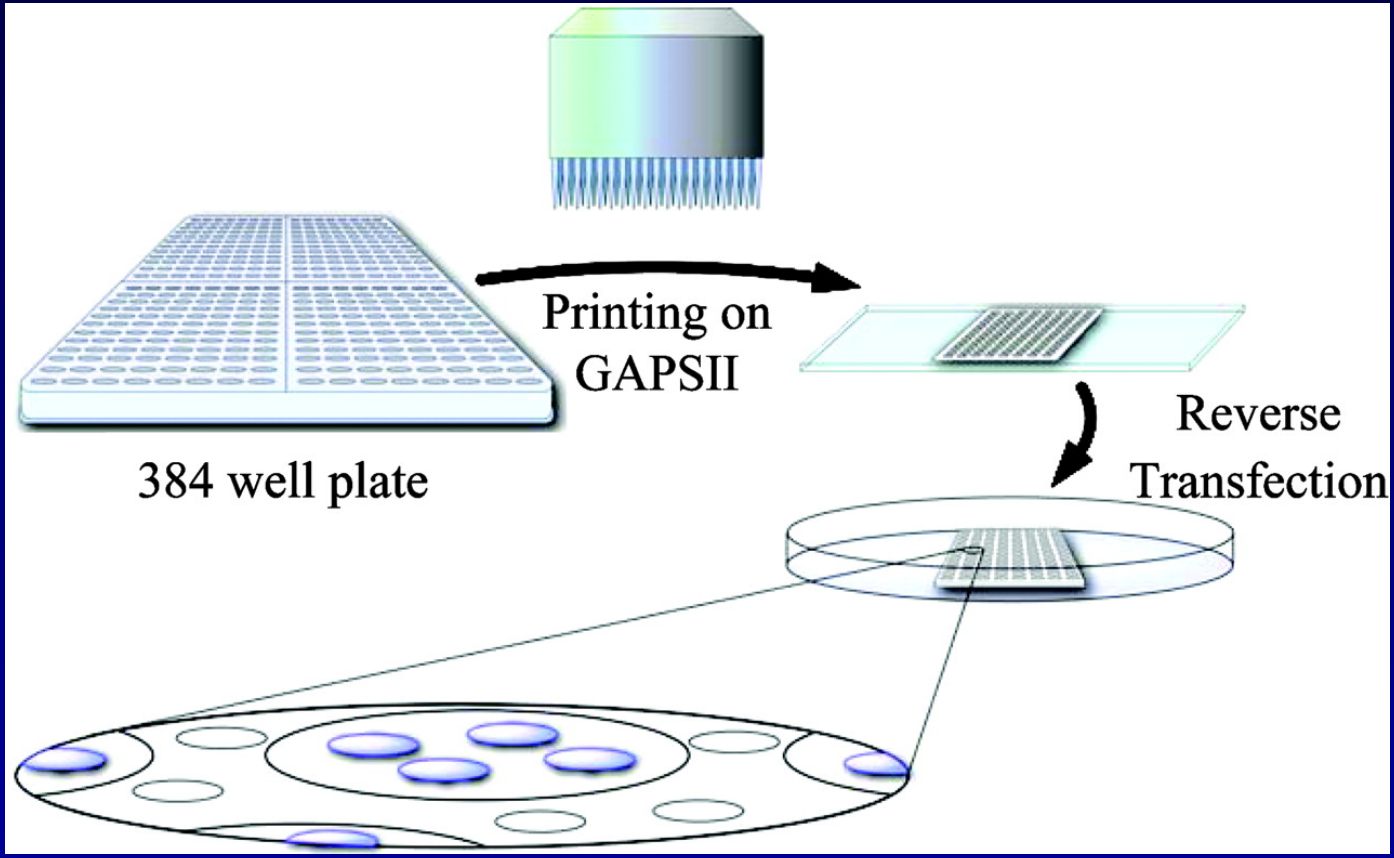
Cell based assays using reverse transfection of RNAi

Fig. 1. Outline of the protocol used to perform reverse transfection on a glass slide



Silva, Jose M. et al. (2004) Proc. Natl. Acad. Sci. USA 101, 6548-6552